

**In the Specification:**

Kindly amend the application to read as follows, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents.

Please delete the paragraph on page 8, line 3, and replace it with the following paragraph:

C1 Figure 9 depicts expression of 1XBSGFP and 1XBMRFP in onion peels. The oligonucleotides are shown in SEQ ID NOS 30 & 31, respectively.

Please delete the paragraph on page 11, line 8, through page 12, line 2, and replace it with the following paragraph:

In a preferred aspect of the present invention, zinc finger nucleic acid binding motifs may be represented as motifs having the following primary structure:

(B)  $X^a \text{C } X_{2-4} \text{C } X_{2-3} \text{F } X^c \text{X X X L X X H X X } X^b \text{H} - \text{linker}$  (SEQ ID NO: 22)

C2 wherein X (including  $X^a$ ,  $X^b$  and  $X^c$ ) is any amino acid.  $X_{2-4}$  and  $X_{2-3}$  refer to the presence of 2 or 4, or 2 or 3, amino acids, respectively, and  $\text{X X X X L X X H X X}$  between  $X^c$  and  $X^b$  are designated position -1, 1, 2, 3, 4, 5, 6, 7, 8, and 9. The Cys and His residues, which together co-ordinate the zinc metal atom, are marked in bold text and are usually invariant, as is the Leu residue at position +4 in the  $\alpha$ -helix.

Please delete the paragraph on page 13, line 3, and replace it with the following paragraph:

C3 Preferably, the linker is T-G-E-K (SEQ ID NO: 23) or T-G-E-K-P (SEQ ID NO: 24).

Please delete the paragraph on page 15, lines 5-9, and replace it with the following paragraph:

C4 Consensus zinc finger structures may be prepared by comparing the sequences of known zinc fingers, irrespective of whether their binding domain is known. Preferably, the consensus structure is selected from the group consisting of the consensus structure P Y K C P E C G K S F S Q K S D L V K H Q R T H T G (SEQ ID NO: 25), and the consensus structure P Y K C S E C G K A F S Q K S N L T R H Q R I H T G E K P (SEQ ID NO: 26).

Please delete the paragraph on page 15, lines 10-15, and replace it with the following paragraph:

C5 The consensuses are derived from the consensus provided by Krizek *et al.*, (1991) J. Am. Chem. Soc. 113: 4518-4523 and from Jacobs, (1993) PhD thesis, University of Cambridge, UK. In both cases, the linker sequences described above for joining two zinc finger motifs together, namely TGEK (SEQ ID NO: 23) or TGEKP (SEQ ID NO: 24) can be formed on the ends of the consensus. Thus, a P may be removed where necessary, or, in the case of the consensus terminating T G, E K (P) can be added.

Please delete the paragraph on page 19, lines 5-6, and replace it with the following paragraph:

C6 A "leader" peptide may be added to the N-terminal finger. Preferably, the leader peptide is MAEEKP (SEQ ID NO: 27).

Please delete the paragraph on page 52, lines 16-22, and replace it with the following paragraph:

C7 The DNA binding site for the TFIIIAZif protein contains the DNA recognition sites for zinc fingers 1-3 of TFIIIA and the three zinc fingers of Zif 268. These are the DNA sequences GGATGGGAGAC (SEQ ID NO: 32) and GCGTGGGCGT (SEQ ID NO: 33), respectively. The six base pair sequence GTACCT in Sequence ID NO:3 is a spacer region of DNA that separates the two binding sites and the nucleotide composition of the DNA spacer appears to have no effect on binding of the protein. Therefore, this or other structured linkers could be used with other DNA spacers of different length and sequence.

Please delete the paragraph on page 53, lines 1-3, and replace it with the following paragraph:

C8 The amino acid sequence of zinc Finger 4 of TFIIIA, including the flanking sequences as used in the composite protein of the invention, is

NIKICVYVCHFENCGKAFKKHNQLK VHQFSHTQQLP (SEQ ID NO: 28).

Please delete the paragraph on page 53, lines 4-6, and replace it with the following paragraph:

C9 The nucleotide Sequence of Zinc Finger 4 of TFIIIA, including the flanking sequences, is  
AACATCAAGATCTGCGTCTATGTGTGCCATTTGAGAACTGTGGCAAAGCATTCAAGAA  
ACACAATCAATTAAAGGTTTCATCAGTTCAGTCACACACAGCAGCTGCCG (SEQ ID NO: 29).

Please replace the previously filed sequence listing with the enclosed pages entitled "Sequence Listing".

**In the Claims:**

Please amend the claims without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents.

26. (Amended) The plant host cell or transgenic plant of claim 25 wherein the zinc finger structures have a binding motif represented by:

C10  $X^a C X_{2-4} C X_{2-3} F X^c X X X L X X H X X X^b H$  – linker (SEQ ID NO: 22)  
wherein each of X,  $X^a$ ,  $X^b$ ,  $X^c$  is any amino acid, the numbers in subscript indicate possible numbers of residues, and X X X X L X X H X X between  $X^c$  and  $X^b$  are designated positions -1, 1, 2, 3, 4, 5, 6, 7, 8, and 9.

27. (Amended) The plant host cell or transgenic plant of claim 26 wherein  $X^a$  is E, K, T, S, Q, V, A or P,  $X^b$  is T or I,  $X^c$  is S or T,  $X_{2-4}$  is two amino acids, with the first of which being S, E, K, T, P, or R, and the second amino acid being E, and the linker is T-G-E-K (SEQ ID NO: 23) or T-G-E-K-P (SEQ ID NO: 24), and position 9 is Arg or Lys, and positions 1, 5, and 8 are hydrophobic amino acids and not Phe, Trp or Tyr.

C11 29. (Amended) The plant host cell or transgenic plant of claim 26 wherein there is an N-terminal zinc finger having a leader peptide MAEEKP (SEQ ID NO: 27) added thereto.

53. (Amended) The method of claim 52 wherein the zinc finger structures have a binding motif represented by:

$X^a C X_{2-4} C X_{2-3} F X^c X X X X L X X H X X X^b H$  – linker (SEQ ID NO: 22)

C12 wherein each of X,  $X^a$ ,  $X^b$ ,  $X^c$  is any amino acid, the numbers in subscript indicated possible numbers of residues, and  $X X X X L X X H X X$  between  $X^c$  and  $X^b$  are designated positions -1, 1, 2, 3, 4, 5, 6, 7, 8, and 9.

54. (Amended) The method of claim 53 wherein  $X^a$  is E, K, T, S, Q, V, A or P,  $X^b$  is T or I,  $X^c$  is S or T,  $X_{2-4}$  is two amino acids, with the first of which being S, E, K, T, P, or R, and the second amino acid being E, and the linker is T-G-E-K (SEQ ID NO: 23) or T-G-E-K-P (SEQ ID NO: 24), and position 9 is Arg or Lys, and positions 1, 5, and 8 are hydrophobic amino acids and not Phe, Trp or Tyr.

C13 56. (Amended) The method of claim 53 wherein there is an N-terminal zinc finger having a leader peptide MAEEKP (SEQ ID NO: 27) added thereto.